

Query Match 60.3%; Score 622; DB 2; Length 204;  
Best Local Similarity 58.5%; Pred. No. 3.6e-45;  
Matches 117; Conservative 35; Mismatches 48; Indels 0; Gaps 0;

Qy 1  
MFKFLKRVVFLAFLIFCFYQAYITHQNVQNVMQYKPMVEKTLAENDTTANVNL  
VLAMIYT 60

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Db 1  
MFKRIRRVLVLAFLFAGYKAYRVHQDVKQVMQYQPMVREILSEQDTPANEEL  
VLAMIYT 60

Qy 61  
ETKGGQADVMQSSSESSSGVTNSITDSQSSIQHGVKLLSENLTAEKAGVDSWTA  
VQAYNF 120

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Db 61  
ETKKGEGDVMQSSSESASGSTNTINDNASSIRQGIQTLTGNNLYLAQKKGVDIWTAV  
QAYNF 120

Qy 121  
GTAYIDYVAKNGGDNTISLASHYSKSVVAPSLGNKDGKMYLYYHPIALLYGGKL  
YQNGGN 180

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Db 121  
GPAYIDFIAQNGKENTLALAKQYSRETVAPLLGNRTGKTYSYIHPISIFHGAELYV  
NGGN 180

Qy 181 IYYSREVHFNYLIQLLSKF 200

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Db 181 YYYSRQVRLNLYIHKCFTLF 200